

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/993,962

1642
#ef
DATE: 05/22/98
TIME: 14:11:26

INPUT SET: S3072.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia

(ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: US
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Macintosh 7.0.1
(D) SOFTWARE: Microsoft Word, Version #5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/993,962
(B) FILING DATE: December 18, 1997
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/162,407
(B) FILING DATE: December 3, 1993

(A) APPLICATION NUMBER: 08/111,758
(B) FILING DATE: August 25, 1993
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/106,463
(B) FILING DATE: August 12, 1993
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/068,394
(B) FILING DATE: May 24, 1993

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/993,962

DATE: 05/22/98
TIME: 14:11:27

INPUT SET: S3072.raw

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Malaska, Stephen L.
(B) REGISTRATION NUMBER: 32,655
(C) REFERENCE/DOCKET NUMBER: 2813-C

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (206) 587-0430
(B) TELEFAX: (206) 233-0644
(C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..25

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 855..879

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

88	GTG	ACT	GGA	ACG	AGC	GAC	CTG	CTC	TGT	AC	AGG	CAT	GGA	GGG	GTC	CCCG	GC	AGAG	56
89																			
90	ATG	ACA	GTG	CTG	GCG	CCA	GCC	TGG	AGC	CCA	AAT	TCC	TCC	CTG	TTG	CTG		104	
91	Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Asn	Ser	Ser	Leu	Leu	Leu			
92	1				5					10					15				
93																			
94	CTG	TTG	CTG	CTG	CTG	AGT	CCT	TGC	CTG	CGG	GGG	ACA	CCT	GAC	TGT	TAC	152		
95	Leu	Leu	Leu	Leu	Leu	Ser	Pro	Cys	Leu	Arg	Gly	Thr	Pro	Asp	Cys	Tyr			
96					20				25					30					
97	TTC	AGC	CAC	AGT	CCC	ATC	TCC	TCC	AAC	TTC	AAA	GTG	AAG	TTT	AGA	GAG	200		
98	Phe	Ser	His	Ser	Pro	Ile	Ser	Ser	Asn	Phe	Lys	Val	Lys	Phe	Arg	Glu			
99					35				40					45					

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/993,962*

DATE: 05/22/98
TIME: 14:11:29

INPUT SET: *S3072.raw*

101	TTG	ACT	GAC	CAC	CTG	CTT	AAA	GAT	TAC	CCA	GTG	ACT	GTG	GCC	GTG	AAT	
102	Leu	Thr	Asp	His	Leu	Leu	Lys	Asp	Tyr	Pro	Val	Thr	Val	Ala	Val	Asn	248
103		50					55					60					
104																	
105	CTT	CAG	GAC	GAG	AAG	CAC	TGC	AAG	GCC	TTG	TGG	AGC	CTC	TTC	CTA	GCC	296
106	Leu	Gln	Asp	Glu	Lys	Cys	Lys	Lys	Ala	Leu	Trp	Ser	Leu	Phe	Leu	Ala	
107	65					70					75					80	
108																	
109	CAG	CGC	TGG	ATA	GAG	CAA	CTG	AAG	ACT	GTG	GCA	GGG	TCT	AAG	ATG	CAA	344
110	Gln	Arg	Trp	Ile	Glu	Gln	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	
111					85					90					95		
112																	
113	ACG	CTT	CTG	GAG	GAC	GTC	AAC	ACC	GAG	ATA	CAT	TTT	GTC	ACC	TCA	TGT	392
114	Thr	Leu	Leu	Glu	Asp	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Ser	Cys	
115				100					105					110			
116																	
117	ACC	TTC	CAG	CCC	CTA	CCA	GAA	TGT	CTG	CGA	TTC	GTC	CAG	ACC	AAC	ATC	440
118	Thr	Phe	Gln	Pro	Leu	Pro	Glu	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	
119			115					120					125				
120																	
121	TCC	CAC	CTC	CTG	AAG	GAC	ACC	TGC	ACA	CAG	CTG	CTT	GCT	CTG	AAG	CCC	488
122	Ser	His	Leu	Leu	Lys	Asp	Thr	Cys	Thr	Gln	Leu	Leu	Ala	Leu	Lys	Pro	
123		130					135					140					
124																	
125	TGT	ATC	GGG	AAG	GCC	TGC	CAG	AAT	TTC	TCT	CGG	TGC	CTG	GAG	GTG	CAG	536
126	Cys	Ile	Gly	Lys	Ala	Cys	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Val	Gln	
127	145					150					155					160	
128																	
129	TGC	CAG	CCG	GAC	TCC	TCC	ACC	CTG	CTG	CCC	CCA	AGG	AGT	CCC	ATA	GCC	584
130	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Leu	Pro	Pro	Arg	Ser	Pro	Ile	Ala	
131					165					170					175		
132																	
133	CTA	GAA	GCC	ACG	GAG	CTC	CCA	GAG	CCT	CGG	CCC	AGG	CAG	CTG	TTG	CTC	632
134	Leu	Glu	Ala	Thr	Glu	Leu	Pro	Glu	Pro	Arg	Pro	Arg	Gln	Leu	Leu	Leu	
135				180					185					190			
136																	
137	CTG	CTG	CTG	CTG	CTG	CCT	CTC	ACA	CTG	GTG	CTG	CTG	GCA	GCC	GCC	TGG	680
138	Leu	Leu	Leu	Leu	Pro	Pro	His	Thr	Leu	Val	Leu	Leu	Ala	Ala	Ala	Trp	
139			195					200					205				
140																	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/993,962

DATE: 05/22/98
TIME: 14:11:30

INPUT SET: S3072.raw

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153 (2) INFORMATION FOR SEQ ID NO:2:
154
155 (i) SEQUENCE CHARACTERISTICS:
156 (A) LENGTH: 231 amino acids
157 (B) TYPE: amino acid
158 (D) TOPOLOGY: linear
159
160 (ii) MOLECULE TYPE: protein
161
162
163 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
164
165 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
166 1 5 10 15
167
168 Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
169 20 25 30
170
171 Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
172 35 40 45
173
174 Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
175 50 55 60
176
177 Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
178 65 70 75 80
179
180 Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
181 85 90 95
182
183 Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
184 100 105 110
185
186 Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
187 115 120 125
188
189 Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
190 130 135 140
191
192 Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
193 145 150 155 160
194
195 Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
196 165 170 175
197
198 Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
199 180 185 190
200
201 Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
202 195 200 205
203
204 Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
205 210 215 220

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/993,962DATE: 05/22/98
TIME: 14:11:32

INPUT SET: S3072.raw

206
207 Val Pro Leu Pro Ser His Pro
208 225 230
209
210 (2) INFORMATION FOR SEQ ID NO:3:
211
212 (i) SEQUENCE CHARACTERISTICS:
213 (A) LENGTH: 24 base pairs
214 (B) TYPE: nucleic acid
215 (C) STRANDEDNESS: single
216 (D) TOPOLOGY: linear
217
218 (iii) HYPOTHETICAL: NO
219
220 (iv) ANTI-SENSE: NO
221
222 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
223
224 TCGACTGGAA CGAGACGACC TGCT
225
226
227 (2) INFORMATION FOR SEQ ID NO:4:
228
229 (i) SEQUENCE CHARACTERISTICS:
230 (A) LENGTH: 20 base pairs
231 (B) TYPE: nucleic acid
232 (C) STRANDEDNESS: single
233 (D) TOPOLOGY: linear
234
235 (iii) HYPOTHETICAL: NO
236
237 (iv) ANTI-SENSE: NO
238
239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
240
241 AGCAGGTCGT CTCGTTCCAG
242
243 (2) INFORMATION FOR SEQ ID NO:5:
244
245 (i) SEQUENCE CHARACTERISTICS:
246 (A) LENGTH: 988 base pairs
247 (B) TYPE: nucleic acid
248 (C) STRANDEDNESS: single
249 (D) TOPOLOGY: linear
250
251 (ii) MOLECULE TYPE: cDNA to mRNA
252
253 (iii) HYPOTHETICAL: NO
254
255 (iv) ANTI-SENSE: NO
256
257 (ix) FEATURE:
258 (A) NAME/KEY: CDS

24

20

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/993,962

DATE: 05/22/98
TIME: 14:11:34

INPUT SET: S3072.raw

Line	Error	Original Text
28	Wrong Classification	(C) CLASSIFICATION:435

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/08/993,962*

DATE: 05/22/98
TIME: 14:11:34

INPUT SET: S3072.raw

<< THERE ARE NO ITEMS MISSING >>